

RESULT 1

HUMDAF

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

HUMDAF 2017 bp mRNA linear PRI 02-NOV-1994  
Human complement decay-accelerating factor (DAF) mRNA; 3' end.  
M15799  
M15799.1 GI:181462  
complement decay-accelerating factor.  
Human HeLa cell cDNA to mRNA, clones DF1 and DF2.  
Homo sapiens  
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;  
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo  
1 (bases 1 to 2017)  
Medof, M E , Lublin, D M , Holers, V M , Ayers, D J , Getty, R R ,  
Leykam, J F , Atkinson, J P and Tykocinski, M L  
Cloning and characterization of cDNAs encoding the complete



2003

us-09

Feb 24 11:03:01 2003

Qy 1561 GCAAAATTGCTAAAGAGAGATGACCACATTATAAAGTAATCTTTGGCTAAGGCATTTTCA 1620  
Db 1561 GCAAAATTGCTAAAGAGAGATGACCACATTATAAAGTAATCTTTGGCTAAGGCATTTTCA 1620  
Qy 1621 TCTTTCCTTCGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGTGTG 1680  
Db 1621 TCTTTCCTTCGGTTGGCAAAATATTTTAAAGGTAAAACATGCTGGTGAACCAGGGTGTG 1680  
Qy 1681 ATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTGTGACACAAATAGA 1740  
Db 1681 ATGGTGATAAGGGAGGAATATAGAATGAAAGACTGAATCTTCCTTGTGACACAAATAGA 1740  
Qy 1741 GTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGA 1800  
Db 1741 GTTTGGAAAAAGCCTGTGAAAGGTGTCTTCTTTGACTTAATGTCTTTAAAAGTATCCAGA 1800  
Qy 1801 GATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATA 1860  
Db 1801 GATACTACAATATTAACATAAGAAAAGATTATATATTATTTCTGAATCGAGATGTCCATA 1860  
Qy 1861 GTCAAATTTGTAAATCTTATTCTTTTGTAAATATTTATTTATATTTATTTATGACAGTGAA 1920  
Db 1861 GTCAAATTTGTAAATCTTATTCTTTTGTAAATATTTATTTATATTTATTTATGACAGTGAA 1920  
Qy 1921 CATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTAT 1980  
Db 1921 CATTCTGATTTTACATGTAAAACAAGAAAAGTTGAAGAAGATATGTGAAGAAAAATGTAT 1980  
Qy 1981 TTTTCCTAAATAGAAATAAATGATCCCATTTTGGT 2017  
Db 1981 TTTTCCTAAATAGAAATAAATGATCCCATTTTGGT 2017

ALIGNMENTS

RESULT 1  
HUMDAFA  
LOCUS HUMDAFA 2220 bp mRNA linear PRI 02-NOV-1994  
DEFINITION Human decay-accelerating factor mRNA, complete cds.  
ACCESSION M30142  
VERSION M30142.1 GI:181464  
KEYWORDS Alu repeat; alternative splicing; decay-accelerating factor;  
membrane glycoprotein.  
SOURCE Homo sapiens cDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2220)  
AUTHORS Caras, I.W., Davitz, M.A., Rhee, L., Weddell, G., Martin, D.W. Jr. and  
Nussenzweig, V.

**TITLE** Cloning of decay-accelerating factor suggests novel use of splicing to generate two proteins

**JOURNAL** Nature 325 (6104), 545-549 (1987)

**MEDLINE** 87115845

**PUBMED** 2433596

**COMMENT** The gene for decay accelerating factor produces two proteins by alternative splicing. The spliced out region is from position 1147-1265. The stop codon in this case is located at position 1327-1329. Though mRNAs do not have introns, the alternative coding region is indicated in the features table.

**FEATURES**

**source**

1. 2220

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/map="1q32"

/cell\_line="Hela"

<1. 2220

**mRNA**

/gene="DAF"

/note="G00-119-088"

join(66. 1146, 1265. 1329)

/gene="DAF"

join(66. 1146, 1265. 1329)

/gene="DAF"

/codon\_start=1

/product="decay-accelerating factor A"

/protein\_id="AA52168.1"

/db\_xref="GI:181465"

/db\_xref="GDB:G00-119-088"

/translation="MTVAPSPVPAALPLLGLPRLLLVLCLEPAVWGDCGLPDPVPLNSASLKPQYITQNYFPVGVVEYECRPGYRREPSPKLTCLONLKMSTAVEPCKKSCPNPGEIRNGQIDVPGGILFGATISFCNTGKLFSSFCILSGSSVQWSDPLPSCPEPCRGKSLTSKVPPTVOKPTVNPTEVSPSTOKTTTTPNAQATSTPVSRTKHHEHTTPNKGSGTSTRLLSGHTCFTLGLGLVMTGLLT"

66. 167

**sig\_peptide**

/gene="DAF"

/note="G00-119-088"

join(168. 1146, 1265. 1326)

/gene="DAF"

/product="decay-accelerating factor A"

/note="G00-119-088"

<66. 1146

**exon**

/gene="DAF"

/note="decay-accelerating factor precursor A"

/number=1

168. 1385

/gene="DAF"

/product="decay-accelerating factor A"

/note="G00-119-088"

1147. 1264

**mat\_peptide**

/gene="DAF"

/note="G00-119-088"

1150. 1264

**intron**

/note="Alu repeat (partial)"

1265. >1329

**repeat\_region**

/gene="DAF"

/note="G00-119-088"

/number=2

1410. 1415

/gene="DAF"

/note="G00-119-088; putative"

1693. 1698

**polyA\_signal**

/gene="DAF"

/note="G00-119-088; putative"

1731. 1736

**polyA\_signal**

/gene="DAF"

/note="G00-119-088; putative"

2198. 2203

**polyA\_signal**

/gene="DAF"

/note="G00-119-088; putative"

2220

**BASE COUNT** 681 a 455 c 475 g 609 t

**ORIGIN**

Query Match 100.0%; Score 2220; DB 9; Length 2220; Best Local Similarity 100.0%; Pred. No. 0; Matches 2220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGCTGGCGCTAGCTGCGACTCGCGGAGTCCCGCGCGCTCTTGTCTAACCCGGC 60

DB 1 CCGCTGGCGCTAGCTGCGACTCGCGGAGTCCCGCGCGCTCTTGTCTAACCCGGC 60

QY 61 GCGCCATGACCGTCCGCGCGCGGAGCGTCCCGCGCGCTCTTGTCTAACCCGGC 60

DB 61 GCGCCATGACCGTCCGCGCGCGGAGCGTCCCGCGCGCTCTTGTCTAACCCGGC 60

QY 121 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

DB 121 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

QY 181 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

DB 181 CCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180

QY 241 CTGTAATAACGTACCAATGTGAAGAAAGCTTTGTGAATAATCTCGCGAGAGT 240

DB 241 CTGTAATAACGTACCAATGTGAAGAAAGCTTTGTGAATAATCTCGCGAGAGT 240

QY 301 TGATCTGCTTAAGGCGAGTCAATGTGATATTTGAAGAGTCTCTCAATCTGCTG 300

DB 301 TGATCTGCTTAAGGCGAGTCAATGTGATATTTGAAGAGTCTCTCAATCTGCTG 300

QY 361 AGTGCCCAACAGGCTAAATCTGATCTCCCTCAACAGCTTATATCAGTCAAGT 420

DB 361 AGTGCCCAACAGGCTAAATCTGATCTCCCTCAACAGCTTATATCAGTCAAGT 420

QY 421 TTCAGTGGTACTGTTGTGAATATGAGTGGCGTCCAGGTTACAGAGAACTTCTC 480

DB 421 TTCAGTGGTACTGTTGTGAATATGAGTGGCGTCCAGGTTACAGAGAACTTCTC 480

QY 481 TATCACCACCAACTACTGCTTCCCTCAGAAATTTAAATGGTCCACAGCTGCA 540

DB 481 TATCACCACCAACTACTGCTTCCCTCAGAAATTTAAATGGTCCACAGCTGCA 540

QY 541 AAAAGAAATCATGCCCTATCCCGGAGAAATACGAAATGTGATGATGATGATG 600

DB 541 AAAAGAAATCATGCCCTATCCCGGAGAAATACGAAATGTGATGATGATGATG 600

QY 601 GCATATATTTGGTGAACCATCTCTCTCATGTAAACAGGTTACCAATTTTGGCT 660

DB 601 GCATATATTTGGTGAACCATCTCTCTCATGTAAACAGGTTACCAATTTTGGCT 660

QY 661 CGACTTCTAGTTTGTCTTATTTTCCAGGAGCTGCTGCTGCTGCTGCTGCTGCT 720

DB 661 CGACTTCTAGTTTGTCTTATTTTCCAGGAGCTGCTGCTGCTGCTGCTGCTGCT 720

QY 721 AGTGACAGAAATTTATTTGTCAGACCAACCAAAATTTGACATGCAATTAATCA 780

DB 721 AGTGACAGAAATTTATTTGTCAGACCAACCAAAATTTGACATGCAATTAATCA 780

QY 781 AACGTGACCAATTTATTTATTTGTCAGACCAACCAAAATTTGACATGCAATTA 840

DB 781 AACGTGACCAATTTATTTATTTGTCAGACCAACCAAAATTTGACATGCAATTA 840

QY 841 TGATTTGAGAGCACTCTATTTATTTGTCAGTGAATATGAGAGAGTGGGCTG 900

DB 841 TGATTTGAGAGCACTCTATTTATTTGTCAGTGAATATGAGAGAGTGGGCTG 900

QY 901 CACCACTGAATGAGAGAAATCTCTAATCTCAAGTCCACCAAGTTCAGAAC 960

DB 901 CACCACTGAATGAGAGAAATCTCTAATCTCAAGTCCACCAAGTTCAGAAC 960

QY 961 CTACCAAGTAATGTTCCAACTACAGAGTCTCACCACCTCTCAGAAACACCA 1020



```
|||||
Db 961 CTACCACAGTAAATGTTCCAACTACAGAACTCTCACCAACTTCTCAGAAAAACACCAAA 1020
QY 1021 AAACCAACCACCAAAATGCTCAAGCAACACGAGTACACTGTCTCCAGACAACCAAGC 1080
|||||
Db 1021 AAACCAACCACCAAAATGCTCAAGCAACACGAGTACACTGTCTCCAGACAACCAAGC 1080
QY 1081 ATTTTCATGAACAACCCCAATTAAGGAAGTGAACCACTTCAGGTACTACCCTCTTC 1140
|||||
Db 1081 ATTTTCATGAACAACCCCAATTAAGGAAGTGAACCACTTCAGGTACTACCCTCTTC 1140
|||||
QY 1141 TATCTGGTCTCTCGTCTGTCACCCAGGCTGTATGCGGTGTGTGATCGTAGCTCACTGC 1200
|||||
Db 1141 TATCTGGTCTCTCGTCTGTCACCCAGGCTGTATGCGGTGTGTGATCGTAGCTCACTGC 1200
QY 1201 AGTCTCGAAGTCTCTGGGTTCAAGCCATCCTTCCACTTCAGCCTCCCAAGTAGCTGTACT 1260
|||||
Db 1201 AGTCTCGAAGTCTCTGGGTTCAAGCCATCCTTCCACTTCAGCCTCCCAAGTAGCTGTACT 1260
QY 1261 ACAGGGCACACAGTGTTCACGTTGACAGGTTTGCTTGGAGGCTAGTAACCATGGGCTTG 1320
|||||
Db 1261 ACAGGGCACACAGTGTTCACGTTGACAGGTTTGCTTGGAGGCTAGTAACCATGGGCTTG 1320
QY 1321 CTGACTTAGCCAAAGAGAGTTAAGAGAAATACACACAAGTATACAGACTGTTCCTAG 1380
|||||
Db 1321 CTGACTTAGCCAAAGAGAGTTAAGAGAAATACACACAAGTATACAGACTGTTCCTAG 1380
QY 1381 TTCTCTAGACTTATCTGCATATTGATAAATTAATGCAATTGTGCTCTTCATTTAGGAT 1440
|||||
Db 1381 TTCTCTAGACTTATCTGCATATTGATAAATTAATGCAATTGTGCTCTTCATTTAGGAT 1440
QY 1441 GCTTTCATGTCTTTAAGATGTGTAGGAATGTCAACAGACCAAGAGAGAAAAAGGCAGT 1500
|||||
Db 1441 GCTTTCATGTCTTTAAGATGTGTAGGAATGTCAACAGACCAAGAGAGAAAAAGGCAGT 1500
QY 1501 CCTGGAATCACATTTCTTAGCACACCTACACCTCTTGAAAAATAGAACAACTTGCAGAAATTG 1560
|||||
Db 1501 CCTGGAATCACATTTCTTAGCACACCTACACCTCTTGAAAAATAGAACAACTTGCAGAAATTG 1560
QY 1561 AGAGTGATTCCTTTCTTAAAGTGTAAAGAAAGCATAGAGATTTGTCGTATTTAGAATGG 1620
|||||
Db 1561 AGAGTGATTCCTTTCTTAAAGTGTAAAGAAAGCATAGAGATTTGTCGTATTTAGAATGG 1620
QY 1621 GATCAGGAGGAAAAAGAGAAAGTATTTTCCACAAGATCTGTAATGTATTTC 1680
|||||
Db 1621 GATCAGGAGGAAAAAGAGAAAGTATTTTCCACAAGATCTGTAATGTATTTC 1680
QY 1681 ACTTATAAGGAAATTAATAATGAAAAACATTTTGGATATCAAAAGCAAAATTAATAAAC 1740
|||||
Db 1681 ACTTATAAGGAAATTAATAATGAAAAACATTTTGGATATCAAAAGCAAAATTAATAAAC 1740
QY 1741 CAATTCAGTCTCTTCTAAGCAAAATGCTTAAGAGAGATGAACCATTTATAAGTAATC 1800
|||||
Db 1741 CAATTCAGTCTCTTCTAAGCAAAATGCTTAAGAGAGATGAACCATTTATAAGTAATC 1800
QY 1801 TTTGGCTGTAAGGCATTTTCATCTTTCCTGCGGTTGGCAAAATATTTTAAAGGTAATAAC 1860
|||||
Db 1801 TTTGGCTGTAAGGCATTTTCATCTTTCCTGCGGTTGGCAAAATATTTTAAAGGTAATAAC 1860
QY 1861 ATGCTGGTGAACCAAGGGGTGTGATGTTGAAGAAAGCCCTGTGAAGGTTCTTCTTGGACT 1920
|||||
Db 1861 ATGCTGGTGAACCAAGGGGTGTGATGTTGAAGAAAGCCCTGTGAAGGTTCTTCTTGGACT 1920
QY 1921 TCTTCCTTTGTTGCACAATAGAGTTTGGAAAAAGCCCTGTGAAGGTTCTTCTTGGACT 1980
|||||
Db 1921 TCTTCCTTTGTTGCACAATAGAGTTTGGAAAAAGCCCTGTGAAGGTTCTTCTTGGACT 1980
QY 1981 TAATGCTTTAAAGTATCCAGAGATACTACAAATATTACATTAAGAAAAAGATTATATATT 2040
|||||
Db 1981 TAATGCTTTAAAGTATCCAGAGATACTACAAATATTACATTAAGAAAAAGATTATATATT 2040
QY 2041 ATTTCTGAATCGAGATGTCCATAGTCAAAATTTGTAAATCTTATCTTTGTAAATATTAT 2100
|||||
```

```
Db 2041 ATTTCTGAATCGAGATGTCCATAGTCAAAATTTGTAAATCTTATCTTTGTAAATATTAT 2100
QY 2101 TTATATTTTATTTATGACAGTGAACATTTCTGATTTTACATGTAAACAGAAAAAGTTGAAG 2160
|||||
Db 2101 TTATATTTTATTTATGACAGTGAACATTTCTGATTTTACATGTAAACAGAAAAAGTTGAAG 2160
QY 2161 AAGATATGTGAAGAAAAATGTATTTTCCFAAATAGAAATAAATGATCCCATTTTGGT 2220
|||||
Db 2161 AAGATATGTGAAGAAAAATGTATTTTCCFAAATAGAAATAAATGATCCCATTTTGGT 2220
```

item: